

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb

<130> 30287P-EP

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> Human

<400> 1

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2

<211> 172

<212> PRT

<213> Human

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val

1	5	10	15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro			
20	25	30	
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr			
35	40	45	
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asp Ser Gly			
50	55	60	
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His			
65	70	75	80
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu			
85	90	95	
Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp			
100	105	110	
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys			
115	120	125	
Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser			
130	135	140	
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr			
145	150	155	160
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro			
165	170		

<210> 3
 <211> 13
 <212> PRT
 <213> Human

<400> 3
 Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
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<210> 4
 <211> 312
 <212> DNA
 <213> hybridoma

<220>
 <221> CDS
 <222> (1)..(312)

<400> 4
 aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
 Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
 20 25 30

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tta	agc	tgg	ctt	cag	cag	aaa	cca	gat	gga	act	att	aaa	cgc	ctg	atc	144
Leu	Ser	Trp	Leu	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Ile	Lys	Arg	Leu	Ile	
35							40					45				
tac	gcc	aca	tcc	gct	tta	gat	tct	ggt	gtc	cca	aaa	agg	ttc	agt	ggc	192
Tyr	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly	
50					55						60					
agt	ggg	tct	ggg	tca	aat	tat	tct	ctc	acc	atc	agc	agc	ctt	gag	tct	240
Ser	Gly	Ser	Gly	Ser	Asn	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser	
65					70					75			80			
gaa	gat	ttt	gca	gac	tat	tac	tgt	cta	caa	tat	gct	aat	tat	ccg	tac	288
Glu	Asp	Phe	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Asn	Tyr	Pro	Tyr	
85								90			95					
acg	ttc	gga	ggg	ggg	acc	aag	ctg									312
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu									
100																

<210> 5

<211> 104

<212> PRT

<213> hybridoma

<400> 5

Arg	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
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Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Glu	Ile	Ser	Gly	Tyr
				20				25				30			

Leu	Ser	Trp	Leu	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Ile	Lys	Arg	Leu	Ile
						35		40			45				

Tyr	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly
				50			55			60					

Ser	Gly	Ser	Gly	Ser	Asn	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser
				65			70			75			80		

Glu	Asp	Phe	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Asn	Tyr	Pro	Tyr
				85				90			95				

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu								
				100											

<210> 6

<211> 312

<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)...(312)

<400> 6

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Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1					5				10			15				

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat	96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr	
20 25 30	
ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga	144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly	
35 40 45	
tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag	192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys	
50 55 60	
gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg	240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Thr Ala Tyr Met	
65 70 75 80	
ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat	288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr	
85 90 95	
ggt ccg ttt gct tac tgg ggc caa	312
Gly Pro Phe Ala Tyr Trp Gly Gln	
100	

<210> 7
 <211> 104
 <212> PRT
 <213> hybridoma

<400> 7	
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser	
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Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr	
20 25 30	
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly	
35 40 45	
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys	
50 55 60	
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Thr Ala Tyr Met	
65 70 75 80	
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr	
85 90 95	
Gly Pro Phe Ala Tyr Trp Gly Gln	
100	

<210> 8
 <211> 331
 <212> DNA
 <213> hybridoma

<220>
 <221> CDS
 <222> (1)...(330)

<400> 8

aga att cag ctg acc cag tct cct gct tcc tta gct gta tct ctg ggg 48
 Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

cag agg gcc acc atc tca tac agg gcc agc aaa agt gtc agt aca tct 96
 Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
 20 25 30

ggc tat agt tat atg cac tgg aac caa cag aaa cca gga cag cca ccc 144
 Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

aga ctc ctc atc tat ctt gta tcc aac cta gaa tct ggg gtc cct gcc 192
 Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60

agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat 240
 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

cct gtg gag gag gat gct gca acc tat tac tgt cag cac att agg 288
 Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
 85 90 95

gag ctt aca cgt tcg gag ggg gga cca agc tgg aga tct aac a 331
 Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
 100 105 110

<210> 9

<211> 110

<212> PRT

<213> hybridoma

<400> 9

Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
 20 25 30

Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
 85 90 95

Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
 100 105 110

<210> 10

<211> 343

<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)..(342)

<400> 10

gtg cag ctg cag gag tct gga cct ggc ctg gtg gcg ccc tca cag agc 48
 Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
 1 5 10 15

ctg tcc atc aca tgc acc gtc tca ggg ttc tca tta act agc tat ggt 96
 Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
 20 25 30

gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gta 144
 Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
 35 40 45

gtg ata tgg agt gat gga agc aca acc tat aat tca gct ctc aaa tcc 192
 Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
 50 55 60

aga ctg agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa 240
 Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
 65 70 75 80

atg aac agt ctc caa act gat gac aca gcc atg tac tac tgt gcc aga 288
 Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95

gag cct ccc acg acg tac gtt tgc tta ctg ggg cca agg gac cac tct 336
 Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
 100 105 110

aga tta a 343
 Arg Leu

<210> 11

<211> 114

<212> PRT

<213> hybridoma

<400> 11

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
 1 5 10 15

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly
 20 25 30

Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val
 35 40 45

Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
 50 55 60

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
 65 70 75 80

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95

Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
100 105 110

Arg Leu